

SEQ ID NO: 6	A33	1	W Y G K W W P V L W T C A V R V T Y D A I S V E T P Q D V L R A S S Q G K S V T L P C T Y H T S T S
SEQ ID NO: 1	40628	1	W G T K A Q V E R A K L L C F I L A I L C S L A L G S V T V H S S E . . . . . P E Y R I P E
SEQ ID NO: 2	45416	1	W G I L G L L G H L T Y D T Y G R P I L E V P E S V T G P W K G D V N L P C T Y O P L
SEQ ID NO: 9	35638	1	W A R S R H R L L L R A Y L G Y H K A Y G F S A P K D Q . . . . . Q V Y T A V E
SEQ ID NO: 10	JAM	1	W G T E G K A G R K L L F L F T S M I L G S I L V Q G K G S V Y T A Q . . . . . S D Y Q V P E
A33	51	S R E G L I Q W O K L L L T H T E R V V I W P F S H N K N Y I H G E L Y K N R V S I S H N A E Q S D A	
40628	43	W N P V K L S C A Y S G F S S P R A V E W K F D Q G O T T R L Y C Y N N K I T A S Y E D R V T F L P T	
45416	47	Q G Y T Q V L Y K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G D V	
35638	43	Y Q E A I L A C K T P K X T V S S R L E W K K L G R S V S F Y Y Q Q T L Q G D F K N R A E M I D F	
JAM	42	N E S I K L T C Y S G F S S P R A V E W K F V Q G S T T A L Y C Y N S Q I T A P Y A D R V T F S S S	
A33	101	S I T I D Q L T H A D O N G T Y E C S V S L . W . . . . . S D L E G N T K S R A V A L L V L V P P S K	
40628	93	G I T F K S Y T R E D T G T Y T C M Y S E . . . . . E G G N S Y G E V K Y K L I V L V P P S K	
45416	97	S L Q L S T L E W D O R S H Y T C E V T W Q T P D G H Q V V A D K I T E L R V Q K L S V S K P T V T	
35638	93	N I R I K N V T R S D O A G K Y R C E V S A P S . . . . . E G G Q N L E E D T Y T L E V L V A P A Y	
JAM	92	G I T F S S Y T R K D O N G E Y T C M Y S E . . . . . E G G Q H Y G E V S I H L T V L V P P S K	
A33	144	P E C C I E G E T I I G N N I Q L T C O S K E G S P T P Q Y S W K R Y N I L N Q E Q . . . . .	
40628	135	P T Y N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I V W P T N . P K S T R A F	
45416	147	T G S G Y G F T V P Q G M B I S L O C A R . G S P P I S Y I W Y K Q Q T N N Q E P . . . . .	
35638	137	P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R I L L E N . P R L G S Q S	
JAM	134	P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S H I L T A D A K K T R A F	

FIG.- 1A

SEQ ID NO: 6 A33 186 . . . PLA Q P A S G Q P V S I K N I S T D T S G Y I C T S S N E E G . . . . . T Q F C N I T Y  
 SEQ ID NO: 1 40628 184 S H S S Y Y L N P T T G E L V F D P L S A S D T G E Y S C E A R N G Y G . . . . . T P M T S H A V  
 SEQ ID NO: 2 45416 188 . . . I K V A T L S T L L F K P A V I A D S G S Y F C T A K G A V G S E Q H S D I V K F V V K D  
 SEQ ID NO: 9 35638 186 T H S S Y T W N T K T G T L Q F N T V S K L D T G E Y S C E A R N S V G . . . . . Y R R C P G K R  
 SEQ ID NO: 10 JAM 184 H N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C O A N G Y G . . . . . T A W R S E A A

A33 227 A V R S P S W H V A L Y Y G I A V G V V A A L I I I G I I I Y C C C C R G K D D N T E D K E D A . . .  
 40628 228 R H E A V E R N H G Y I V A A Y L Y T L I L L G I L V F G ! W F A Y S R G H F O R T K K G T S . . .  
 45416 233 S S K L L K T K T E A P T T W T Y P L K A T S T Y K Q S W D W T T D G Y L G E T S A G P G K S L  
 35638 230 . H Q V D D L H I S G I I A Y V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S . . .  
 JAM 228 H H D A V E L N V G G I V A A V L V T R I L L G L L I F G v W F A Y S R G Y F E T T K K G T A P . .

A33 275 . R P N R E A Y E E P P E Q L R E L S R E E E E D D Y R O E E Q R S T G R E S P D H L D Q  
 40628 275 . . . . . . . . . . S K K V I Y S Q P S A R S E E G E F K O T S S F L V . . . . . . .  
 45416 283 P V F A I I I I S L C C M V V F T W A Y I M L C R K T S Q E H V Y E A R . . . . . . .  
 35638 277 . H S S S K A T T W . S E N V Q W L T P V I P A L W K A A A G G S R G Q E F . . . . . . .  
 JAM 276 . . . . . . . . . . G K K V I Y S Q P S T A S E E G E F K O T S S F L V . . . . . . .

FIG.-1B

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SEQID NO:1

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Cys	Leu	Phe	Ile	Leu	Ala	Ile	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr				
1																															
10																															
15																															
20																															
25																															
30																															
Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro	Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val		
35																															
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45																															
50																															
55																															
60																															
Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Phe	Leu			
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Pro	Thr	Gly	Ile	Thr	Phe	Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr	Gly	Thr	Thr	Cys	Met	Vai	Ser	Glu	Gly	Gly	Asn	Ser	Tyr	Gly				
125																															
130																															
135																															
140																															
145																															
150																															
Glu	Val	Lys	Val	Ile	Val	Leu	Val	Pro	Pro	Ser	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	Pro	Lys	Ser	Thr			
155																															
160																															
165																															
170																															
175																															
180																															
Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Val	Leu	Asn	Pro	Thr	Thr	Gly	Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	Glu	Tyr		
185																															
190																															
195																															
200																															
Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Tyr	Gly	Thr	Pro	Met	Thr	Ser	Asn	Ala	Vai	Arg	Met	Glu	Ala	Vai	Glu	Arg	Asn	Vai	Gly	Val	Val		
215																															
220																															
225																															
230																															
235																															
240																															
Ala	Ala	Val	Val	Thr	Ile	Ile	Leu	Leu	Gly	Ile	Leu	Val	Phe	Gly	Ile	Trp	Rhe	Ala	Tyr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys			
245																															
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3 / 24

**FIG.-2**

SEQ ID NO:2  
 1 MGILGLLLLLL GHLTDTYGR PILEVPESVT GPMKGDVNLP CTYDPLOGCT QVLKWVQR GSDPVTIFLR DSSGDHIQQA KYQGRLKVSH KVPGDVSLQL

101 STLEMDDRSH YTCEVTWQTP DGNQVVRDKI TELRVQKLSV SKPTVTGSG YGFTVPQGMR ISLQCQARGS PPISYIWYKQ QTNNQEPIKV ATLSTLIFKP  
 ^Glycosaminoglycan attachment site

201 AVIADSCSYF CTAKGQVGSE QHSDIVKFW KDSSKLKTK TEAPTTMTYTP LKATSTVKQS WDWTTDMDGY LGETSAGPGK SLPVFAIILIII ISLCCMVFT  
 ^Transmembrane domain

**FIG.\_3**301 MAYIMLCRKT SQEHVYEA AR

OLI2166 (35936.f3)  
 SEQ ID NO:16  
 TTGCCGTTACTCAGGTGCTGCTAC  
 OLI2167 (35936.r2)  
 SEQ ID NO:17  
 ACTCAGCAGTGGACAAGGCGCAAGGAAACTGTTGTGCCT  
 OLI2162 (35936.f1)  
 SEQ ID NO:12  
 TCGCGGAGCTGTTCTGTTTCC  
 OLI2163 (35936.p1)  
 SEQ ID NO:13  
 TGATCGCGATGGGGACAAAGGCGCAAGGAAACTGTTGTGCCT  
 OLI2164 (35936.f2)  
 SEQ ID NO:14  
 ACACCTGGTTCAAAGATGGG  
 OLI2165 (35936.r1)  
 SEQ ID NO:15  
 TAGGAAGTTGCTGAAGGCACGG

**FIG.\_8**

DNA35936 SEQ ID NO:3

CTTCTTGCCA ACTGGTATCA CCTTCAGTC CGTGACACGG GAAGACACTG 50  
 GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGAG 100  
 GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150  
 CATCCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200  
 AACAAAGATGG TTCCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250  
 GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300  
 TGTCCCTGAAT CCCACAAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350  
 CTGATACTGG AGAAATACAGC TGTGAGGCAC GGAATGGGTA 390

**FIG.\_4A**

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50  
 CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100  
 GCGCAAGCTC GAGAGGAAAC TGTTGTGCCT CTTCATATTG GCGATCCTGT 150  
 TGTGCTCCCT GGCATTGGGC AGTGTACAG TTGCACTCTT CTGAACCTGA 200  
 AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCCCTGT GCCTACTCGG 250  
 GCTTTCTTC TCCCCGTGTG GAGTGGAAAGT TTGACCAAGG AGACACCACC 300  
 AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350  
 GACCTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAAGACA 400  
 CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450  
 GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500  
 TAACATCCCC TCCTCTGCCA CCATTGGAA CCGGGCAGTG CTGACATGCT 550  
 CAGAACAAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600  
 ATAGTGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650  
 CTATGTCCCTG AATCCCACAA CAGGAGAGCT GGTCTTGAT CCCCTGTCAG 700  
 CCTCTGATAAC TGGAGAATAC AGCTGT 726

**FIG.\_4B**

consen02 SEQ ID NO:5

GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50  
 ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100  
 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150  
 TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG 200  
 TGACAACCTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250  
 AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300  
 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCTAAG 350  
 TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTCT 400  
 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450  
 TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500  
 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550  
 GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600  
 CCAGGAAAGA GCCTGCCTGT CTTGCCATC ATCCTCATCA TCTCCTTGTG 650  
 CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700  
 CCCAACAAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750  
 AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800  
 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG 850  
 CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900  
 CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950  
 AGGGCAAAAG TGTCTGTTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC 1000  
 ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050  
 CTCTCTTCCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100  
 GGGAGTCACT GGCTTGCCC TGGATTTCAG CAGATGCATC TCAAGTAAGC 1150  
 CAGCTGCTGG ATTTGGCTCT GGGCCCTCT AGTATCTCTG CCGGGGGCTT 1200  
 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250  
 TTGGTCATCA TGCCTACAGA CACTATTCAA CTTGGCATC TTGCCACCAAG 1300  
 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350  
 CAGGATCATT TCTCTTCTT CAGGGCCAGA CAGCTTTAA TTGAAATTGT 1400  
 TATTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450  
 TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500  
 AAA 1503

**FIG.\_4C**

SEQ ID NO:11 CGAGTCCTT CGGGGCTGT TGTGTCAGTG GCCTGATCGC GATGGGACA AAGGCCAAG TCGAGGAA ACTGTGTGC CTCTTCATA 100  
 TGGCGATCCT GTGTCGCTCC CTGGCATTTG CGAGTGTAC AGTGCACCT TCTGAACCTG AAGTCAGAAT TCTTGAGAAT AACCTGTA AGTGTGCTG 200  
 TGCCTACTCG GGCTTTCTT CTCCCCGTGT GGAGTGGAAAG TTGACCAAG GAGACACCAC CAGACTCGTT TGCTTATAATA ACAAGATCAC AGCTTCCTAT 300  
 GAGGACCGGG TAGACCTTCTT GCCAACCTGT ATCACCTCA AGTCCGTGAC ACGGGAAGAC ACTGGACAT ACACCTGTAT GGTCCTGTGAG GAAGGGGGCA 400  
 ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGTGTCTGT GCCTCCATCC AGGCCTACAG TAAACATCCC CTCCCTGTGC ACCATTGGGA ACCGGGCAAGT 500  
 GCTGACATGCA CGAGAACAG ATGGTCCCC ACCTCTGAA TACACTGGT TCAAAGATGG GATACTGTG CCTACGAATIC CAAAAGCAC CGGTGCCTC 600  
 AGCAACTCTT CCTATGTCCT GAATCCACA ACAGGAGGC TGGTCTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG 700  
 GGTATGGAC ACCCATGACT TCAAATGCTG TGGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATGTG GGCAAGCGTC CTGTAAACCC TGATTCTCC 800  
 GGGAAATCTG GTTTGGCA TCTGGTTGC CTATAGCCGA GGCCACTTGG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT 900  
 AGTGCCTGAA GTGAAGGAGA ATTCAACAG ACCTCGTCAT TCCTGTCAT AGCCTGGTG AGCCTGGTG GCTCACGCC TATCATCTGC ATTGCTTA CTCAGGTGCT 1000  
 ACCGGACTCT GGGCCCTGT GTCTGTAGTT TCAAGGATG CCTTATTTGT CTCTACACC CCACAGGGCC CCCTACTCTT TCGGATGTGT TTTAATATT 1100  
 GTCAGCTATG TGGCCCATCC TCCTTCATGC CTCCTCTCC TTTCCTACCA CTGCTGAGTG GCCTGGAACCT TGTGTTAAGT GTTTATCCC CATTCTTTG 1200  
 AGGGATCAGG AGGAAATCCT GGGTATGCC TTGACTTCCC TTCTAAGTAG ACAGCAAAA TGGGGGGT CGCAGGAATIC TGCACCTAAC TGCCACCTG 1300  
 GCTGGCAGGG ATCTTGTAAAT AGGTATCTTG AGCTGGTTC TGGCTCTT CTCCTGTAC TGACGACCAAG GGCAGGCTGT TCTAGAGGG GAATTAGAGG 1400  
 CTAGAGGGC TGAATGGTT GTTGTCAGTG GACACTGGG TCTTCCATC TCTGGGGCC ACTCTCTT GTCTCTCCAT GGGAAATGCC ACTGGGATGCC 1500  
 CTCTGCCCTG TCCCTCTGAA TACAAGCTGA CTGACATTGA CTGTCATGA CTGTCATGT GAAATGGC AGCTCTGGT GTGGAGAGCA TAGTAAATT TCAGAGAACT 1600  
 TGAAGCCAAA AGGATTAAA ACCGCTGCTC TAAAGAAAG AAAACTGGAG GCTGGTCACG CCTGTAATCC CAGAGGCTGA GGAGGGCGA 1700  
 TCACCTGAGG TCGGGAGTTIC GGGATCAGGCC TGACCAACAT GGAGAAACCC TACTGGAAT ACAAGTTAG CCAGGCATGG TGTCATGCC CTGTAGTCCC 1800  
 AGCTGCTCAG GAGCCCTGGCA ACAAGGAGCA AACTCCAGCT CA 1842

**FIG.- 5**

SEQ ID NO:7

1 CCCACGGTC CGCCACGGG TCCCCCAGG GGTCGGCGA CGGCCTCCCCA CCACAGAGG TTTGCTTCA TTGCTAGCA GGAGGCTGGA AGAAAGGACA  
GGTGGCAG GGGGTCCC AGGGCTCC CGAGGGGGCT CGGAGGGGGT AAACCTGGAG AAACCATCGT CCTCCGACCT TCTTCCCTGT

101 GAACCTAGCTC TGGCTGTGAT GGGGATCTTA CTGGGGCTCC TACTCCTGGG GCACCTAACCA CGGCCACACT ATGCCCTCC CACCTGGAA GTGCCAGAGA  
CTTCATCGAG ACCGACACTA CCCCTAGACTA CGGGACACTA CCCCTACAT TAGAAGGGAC ATGAGGACCC CGTGGATTGT CACCTGTGAA TACCCGGAGG GTAGGACCTT CACGGGTCTCT  
1 SEQ ID NO:2 M G I L L G L L C H L T V D T Y G R P I L E V P E S  
^MET

201 CTCCTAACAGG ACCTTGGAAGA GGGGATCTCA ATCTTCCCTG CACCTATGAC CCCCTGGAAG GCTACACCCA ACTCTGGCTG AACCTGGCTGG TACAACGGTCC  
CACATTGTCG ACCGACCTT CCCCTACAT TAGAAGGGAC GTGGATACTG GGGGACCTTC CGATGTCGGCT CGAGAACCCAC TTCAACGGACC ATGTTGGACCC  
29 V T G P W K G D V N L P C T Y D P L Q C Y T Q V L V K W L V Q R G  
62 S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P C  
901 CTCAGACCCCT GTCACCACCT TTCTTACCTGA CTCCTTCTGGA CACCATATCC AGGAGGCAA GTACGGCAA GTACGGCAA CGCCCTCCATG TGAGCCACAA GGTTCCAGGA  
GAGTCTGGGA CAGTGGTAGA AAGATGGCACT GAGAAGACCT CTGGTATAAGG TCCTGGCTTT CATGGTCTCCG GGGGACGTAC ACTCGGTCTT CCAACGGTCT  
95 D V S L Q L S T L E H D R S H Y T C E V T W Q T P D G N Q V V R D  
129 K I T E L R V Q K L S V S K P T V T T C S G Y C F T V P Q G M R I  
162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

**FIG.-6A**

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9 / 24

SEQ ID NO:7 701 ACCTTACTCT TCAAGCCTGC GCTGATAGCC GACTCAGGCC CCTATTTCTG CACTGCCAAG GGCCACGGTC CCTCTGACCA GCACAGGGAC ATNGTGAAGT  
TGGAAATGAGA AGTTCGGAGC CCAACTATCGG CTGACTCCGG GGAAATAACAC GTGACGGTT CCGGTCACAC CGAGACTCGT CGTGTGCTG TAACACTTC  
SEQ ID NO:2 195 T L L F K P A V I A D S C S Y F C T A K C Q V G S E Q H S D I V K F

801 TTGTCGCTAA AGACTCCTCA AGACTACTCA AGACCAAGAAC TGAGCCACCT ACAACCATGA CATAACCCTT CAAGGACACA TCTACAGTGA AGCAGTCCTG  
AACACCACTT TCTACGGACT TTGCGATGACT TCTGCTCTCTG ACTCCCTGGA TCTTGGTACT CTATGGAA CTTCCTGTTG AGATGTCAGT TCGTCAGGAC  
229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W

901 CGACTGGACC ACTGACATGG ATGGCTACCT TGGAGAGGCC AGTGCCTGGGC CAGGAAAGAG CCTCCCTCTC TTTCCTCATCA TCCTCATCAT CTCCCTGTC  
CCTGACCTGG TGAATGTAAC TACCGATCGA ACCTCTCTGG TCACCGACCTGG CCTCCCTCTC GGACGGACAG AACCGGTAGT AGGAGTAGTA GAGGAACACG  
262 D W T T D N D G Y L G E T S A G P G K S L P V F A I I L I I S L C

1001 TGTATGGTC TTTTACCAT GGCCTATATC ATGCTCTCTC CGAGAGACATC CCAACAGAG CATGCTACG AAGCAGCCAG GTAGAGAAGT CTCTCCCTCTT  
ACATACACC AAAATGGTA CGGGATATAG TACGGACAG CCCTCTCTAG CGTTGTTCTC GTACAGATGC TTGTCGGTC CATTCTTCA GAGGGAGAA  
295 C M V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTTGA CCCCGTCCCT GCCCTCAATT TTGATTACTG CCAGGAATG TGGAGGAGG GGGGTGTGGC ACAGACCCAA TCCTTAAGCC GGAGGGCTTC  
GCTAAAAGT GGGCAGGGAA CGGGCAGGGAA AACTATGAC CGTCCCTTAC ACCTCCTTCC CCCACACCCG TGTCTGGCTT ACCATTCCGG CCTCCGGAAAG  
1201 AGGGTCAGGA CATACTGCC TTCCCTCTCT CAGGCACCTT CTGAGTTG AACTTAACCA ACAACTGAGGTTT CCTTAAAT CTAGCTAGAC GGAAAGACGAA  
TCCCAGTCTT GTATGACGG AACGGAGAGA GTCCCTGGAA GACTCCAACA AAACCGGAG ACTTGTGTTT CCTTAAAT CTAGCTAGAC GGAAAGACGAA  
GGTCTTAGG ACCAACATC CTAGCACTAT TAATTAAACCG TTCTTAACCTC CGTCTTAACTC CGTCTTCCCA CCCTTGGTC CCTTAAAT CTAGCTAGAC GGAAAGACGAA  
1301 CCAGAATCCC TGGGGCTCT TCCCTCTCT CAGGCACATGCC ATTAAATGCC AAGAAATTGAG GGAGAAGGGT GGGAAACAG GACCAACGCC CCAAGCTCCCT TCTTATGGT  
CCACCCGAGA ACCCGTATC CGCACATGCC TCTCTGGGT TCTCTGACCC TCTCTGACCC TCTCTGACCC TCTTGGTAC TCCOACCGGT AGAAGGGT ACCTACTCC  
1401 GGTGGGCTCT TGGGGCTAG CGCACATGCC AGAGAGGCC AGCAACTCTGG AGAAACCTGG AGAAACCTGG AGCAACTCTGG TCTCTGACCC TCTTGGTAC TCCOACCGGT AGAAGGGT ACCTACTCC  
CCACCCGAGA ACCCGTATC CGCACATGCC TCTCTGGGT TCTCTGACCC TCTCTGACCC TCTCTGACCC TCTTGGTAC TCCOACCGGT AGAAGGGT ACCTACTCC  
1501 CAACTCCCA GAATCTGCC ACAAACTACT CTGATGACCC CTGATGACCC CTCGATAGGA CAGGAGTACCT CGAGATGAGCC TCTCTGACCC TCTCTGACCC  
GTTGAAGGGT CTTAGACCCG TTGTTGATGA GACTACTCGG GACGTACTTA CGCTCTGACCC TCTCTGACCC GACGTACTTA CGCTCTGACCC TCTCTGACCC

FIG.-6B

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SEQ ID NO:7

1601 GGACACAGTT ATGAGTGGATT CGCCCACTGAG GGCAAAGTG TCTGTTAAA ATGCCCCAT AGCCCAAGAT CTGCTGACAT AATTGGCTAG  
CCTGCTCAA GAGACCTAA TACTCAAAGA CCCGTGACTC CCAGGTGATA AGACAAATTT TACGGGTTAA TCCGGTCTA GACGACTGTA TAAACGGATC

1701 TCAGTCCTG CCTCTGGCAT GGCGTTCTTC CCTGCTTACCT CTCTTCCCTG ATAGCCCCAA GTGTCGGCCCT ACCAACACTG GACCCGCTGG CAGTCAGTGG  
AGTCAAGAAC GCAAGACGTA CGGGAAAG CGAGGATGGA GAGAAGGACC TATCGGGTTT CACAGGGGA TGCTTGAC CTCGGGACCT CTCAGTGACC

1801 CTTTCCCTG GAATTGCCA GATCCATCTC AAGTAAGCCA GCTGGCTGGAT TTGGCTCTGG GCCCTTCTAG TATCTCTGCC GGGGGCTTCT  
GAAACGGAC CTTAAACGGT CTACGTAGAG TTCAATTGGT CGACCGACTA AACCGAGACC CGGGAAAGATC ATAGAGACGG CCCCGAAGA CCATGAGGAG

1901 TCTAAATACC AGAGGAAGA TGCCCCATAGGC ACTAGGACTT GGTCACTATG CCTACAGACA CTTACNACT TTGGCATCTT CCCACCAAA GACCCGAGCC  
AGATTATGG TCTCCCTCTT AGGGTATCG TGATCTGTAA CCACTAGTAC GGATGCTCTG CATAAGTCA AACCGTAGAA CGGGGGCTCTT CTGGGGCTCCC

2001 AGGGCTCAGCT CTGCCAGCTC AGAGGAGCTC CTATATCCAG GATCATTCTT CTTCTTCAG GCCCAGACAG CTTTTAATTG AATTGTTAT TTCAACAGGCC  
TCCGAGTCGA GACGGTCGAG TCTCCTGGTC GATATAGGTC CTAGTAAGCA GAAGGAAGTC CGGGTCTGTC GAAATTAAC TTAAACATA AAGTGTCCC

2101 AGGGTTCACT TCTGCTCCTC CACTATAAGT CTATGCTTCT CACTCTCTCC TGCTGCTCAA TAAATATCTA ATCATACAG C  
TCCCAACTCA AGACGAGGAG CTGATATTCA GATTACAGCA CTGAGAGGG ACCCCAGTT ATTATAGAT TACTATGTC G

**FIG.-6C**

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCGGCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCT  
 CAGAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGCAGGAGCCACCACCGCCTCCTCCT  
 GCTGCTGCTGCGTACCTGGTGGTCGCCCTGGCTATCATAGGCCTATGGGTTTCTGC  
 CCCAAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGGCTATTTAGCCTGCAA  
 AACCCCAAAGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTC  
 CTTGTCTACTATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGA  
 TTTCAATATCCGGATCAAAATGTGACAAGAAGTGTGAGTCGGGAAATATCGTTGTGAAGT  
 TAGTGCCCCATCTGAGCAAGGCCAAACCTGGAAGAGGGATACTGACTCTGGAAAGTATT  
 AGTGGCTCCAGCAGTCCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGT  
 AGAGCTACGATGTCAAGACAAAGAAGGGAACTCAGCTCCTGAATAACACATGGTTAACGA  
 TGGCATCCGTTGCTAGAAATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACAC  
 AATGAATAACAAAATGGAACTCTGCAATTAAACTGTTCCAAACTGGACACTGGAGA  
 ATATTCCGTGAAGCCGCAATTCTGGATATCGCAGGTGTCCTGGAAACGAATGCA  
 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTAGTGAT  
 TTCCGTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTCAAAAGAAC  
 CTCCCTCCAGAAGAGTAATTCTCATCTAAAGCCACGACAATGAGTGAATGTGCAGTG  
 GCTCACGCCTGTAATCCCAGCACTTGGAAAGGCCGCGGGCGGATCACGAGGTCAGGA  
 GTTCTAGACCAGTCTGGCCAATATGGTAAACCCATCTCTACTAAAATACAAAAATTAG  
 CTGGGCATGGTGGCATGTGCCTGCAGTCCAGCTGCTTGGAGACAGGAGAATCACTTGA  
 ACCCGGGAGGCAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGTAA  
 CAGAGCAAGATTCCATCTCAAAAATAAAATAAAATAAAATAACTGGTTTTACC  
 TGTAGAATTCTTACAATAATAGCTTGATATTG

**FIG.\_ 7**

SEQ ID NO:9

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT  
 LEWKKLGRSVSFVYYQQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN  
 LEEDTVTLEVVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD  
 GIRLLENPR  
 LGSQSTNSTSYTMNTKTGTLQFNTVSKLDTGEYSCEARN  
 SVGYRRCPGKRMQVDDLNISGI  
 IAAVVVVALVISVCGLGV  
 CYAQRKGYFSKETS  
 FQKSNSSSKATTMSE  
 NVQWLTPV  
 IPALW  
 KAAAGGSRGQEF

**FIG.\_ 11**

SEQ ID NO:5

1 CGAGGAAAG TACCGGGCCC GCCTCCATGT GAGCCACAG GTTCAGGAG ATGTATCCCT CCAATTGACC ACCCTGGACA TGGATGACCC GAGCCACTAC  
 CGTCCGTTTC ATGGTCCCCG CGAACCTACA CTCGGTCTTC CAGGCTCTC TACATAGGGA CGTTAATCTG TGGACCTCT ACCTACTGGC CTGGCTGATG  
 ^42257 . f1 SEQ ID NO:18 ^42257 . p1 SEQ ID NO:22

101 ACGTGTGAAG TCACCTGGCA GACTCCTCAT GGCACACCAAG TCGTGAGAGA TAAGATTACT GAGCTCGTG TCCAGAACT CTCTGCTCC AAGCCACAG  
 TGCACACTC AGTGGACCGT CTCAGGACTA CGCTGGTTTC AGGACTCTCT ATTCTTAATGA CTCGAGGCAC AGGTCTTTGA GAGACAGGG TTGGCTGTC

201 TGCACACTG CAGGGTTAT GCCTTACGG AGCAGGATT AGCCTTCAT CCCAGGTT CCCAGGTTCC TCCCATCAGT TATATTGGT  
 ACTGTGTAC CTCAGGACTA CGCAAGTGCC ACGGGGTCCC TTACTCCTAA TCGGAAGTTA CGGCAAGAG CCCAAAGG AGGGTAGTCA ATATAACCA

301 ATAAGCAACA GACTATAAC CAGGGAAACC ATCAAAAGTAG CAACCCCTAAC TACCTTACTC TTCAACCTG CGGTGATGCC CGACTCAGGC TCCTATTTCT  
 TATTGTTGT CTGATTATTG CCTCCCTGGG TAGTTTATC GTCAGGATTTC ATGGAATGAA AAGTTGGAC GCCACTATCG GCTGACTCTCG AGGATAAGA

401 GCACTGCCAA GGCCCAAGTT GGCCTCTGAG AGCACAGGA CATTGTGAAG TTTGTGCTCA AAACACTCTC AAAAGCTACTC AAGACCAAGA CTGAGGGACC  
 CGTACGGCTT CCCGGTCAA CGGAGACTCG TCTGTCTGCT GTACACTTC AACACCAAGT TTCTGAGGAG TTTCGATGAG TTCTGGTTCT GACTCCCTGG  
 ^42257 . r1 SEQ ID NO:20

501 TACAACCATG ACATACCCCT TGAAGGCAAC ATCTACAGTG AAGGAGCTCT GGACTCGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGG  
 ATGTTGGTAC TGTATGGGA ACTTTCTCAC TTCCCTAGGA CCTGACCTG GTGACTCTAC CTACCGATGG AACCTCTCTG GTCACGGACCC

601 CCAGGAAAGA CCCTGGCTGT CTTCCTCATCA TCCCTCATCA TCTCTTGTG CTGTATGCTG GTTTCACCA TGCCCTATAT CATGGCTCTGT CGGAAGACAT  
 GGTCTTCTCT CGTACAGATG CTCAGGATAG TAGGAGTAGT AGAGGAACAC GACATACAC CAAAAATGGT ACCGGATATA GTACGGAGACA GCCTCTGTGA  
 ^42257 . f2 SEQ ID NO:19

701 CCCAACAGA GCATGTCTAC GAACCAACCA GGGCACATGC CAGAGGGCC AACACTCTG GAGAAACCAT GAGGGCTGGCC ATCTTCACCA GTGGCTGCTC  
 GGGTCTCTCT CGTACAGATG CTCAGGATAG TAGGAGTAGT AGAGGAACAC GACATACAC CAAAAATGGT ACCGGATATA GTACGGAGACA GCCTCTGTGA  
 ^42257 . f2 SEQ ID NO:19

FIG.- 9A

SEQ ID NO:5  
 801 CAGTGTGAG CCAACTTCCC AGAATCTGGG CCACAACTA CTCTGATGAG CCCCTGCATAG GACAGGAGTA CCAGATCATC GCCCCAAGTCA ATGGCAACTA  
 GTCACTACTC GGTTGAAGGG TCTTAGACCC CGTTGTGAT GAGACTACTC CGGACGTATC CTGTCCTCAT CGTCTAGTAG CGGTCTAGT TACCGTTGAT

901 CGCCCCCTG CTGGACACAG TTTCCTCTGGA TTATGAGTT CTGGCCACTG AGGGCANAAG TGTCGTGTTAA AAATGCCCA TTAGGCCAGG ATCTGGCTGAC  
 GGGGGGGAC GACCTGTGTC AAGGACACCT AATACTCAA GACCCGGTAC TCCCCTTTC ACAGACAATT TTTACGGGT ATCCGGTCC TAGACGACTG

1001 ATAATGGCTT AGTCAGTCTT TGCCTTCTGC ATGGCCCTTCT TCCCTGCTAC CTCTCTTCCCT GGATAGGCCA AAGTGTCCG CTACAAACAC TGGAGGCC  
 TATTAACGGA TCACTCAGGA ACGGAAGACG TACCGGAAGA AGGGACGATG GAGAGAAGGA CCTATCGGGT TTCACAGGG GATGGTTGTG ACCTCGGGCA

1101 CCCAGTCACT GGCTTGGCC TGGMATTGG CAGGATGCCATC TCAAGTAAGC CACCTGCTGG ATTGGCTCT GGCCCTCTCT AGTATCTCTG CCGGGGCTT  
 CCCCTACTGA CGAAAACGGG ACCTTAACGG CTCATACGGT AGTTCTATTG GTCGGACGACC TAAACCGAGA CCCACGAGAC GCATAGACAC GGGCCCCGGAA  
 ^42257.r2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGAGGAA GATGCCATA GCACTAGGAC TTGGTCATCA TGCTACAGA CACTATTCAA CTTCGGCATC TTGCCACCCAG  
 GACCATGAGG AGACATTAT GGTCTCCCTT CTAAAGGTAT CGTGATCCTG AACCTAGT ACCGATGTCT GTGATAAGT GAAACCGTAG AACGGTGGC

1301 AAGACCCGAG GGGAGGCTCA GGTCTGGCAG CTCAGAGGAC CAGCTTATC CAGGATCATT TCTCTTTCTT CAGGGCAGA CAGCTTTAA TTGAAATTCT  
 TTCTGGGCTC CCCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCTAGTAA AGAGAAAGAA GTCCGGCTCT GTCCGAAATT AACTTAACAA

1401 TATTACACAG CCCAGGGTTC AGCTCTGCTC CTCACTATA AGTCTAATGT TCTGACTCTC TCCTGGCTCT CAATAAATCTAATCTAA CAGCAAA  
 ATAAAGTGTGTC CGGTCCCAAG TCAAGACGGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCAACGA GTTATTATA GATTAGTATT GTCCGTTTTT

1501 AAA  
 TTT

**FIG.\_ 9B**

		FRAME	SCORE	MATCH	PCT
A33_HUMAN	A33 ANTIGEN PRECURSOR - HOMO SAPIENS	+1	246	81	30

A33\_HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)

SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19

IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

DNA40628 121 LALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPR---VEW-KFDQGDTTRLVC--YNN  
SEQ ID NO:23

A33\_human 17 VTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHERVVIWPFSN  
SEQ ID NO:24

DNA40628 283 K--ITAS-YEDRVTEI-----PTGITEFKSVTREDTGTYTCMVS---EEGGNSYGEVKVK  
\* \* . \* .. \* \* . \*  
A33\_human 77 KNYIHGELYKNRVSISNNAEQSDASITIDQLTMAADNGTYECCSVSLMSDLEGNT-KSRVR

DNA40628 427 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPPSEYTWFKDGIIVMPTNPKSTRAFSN  
\* . \*  
A33\_human 135 LLVLVPPSKPECIGEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQP-----

DNA40628 607 SSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV---IVA  
\* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \*  
A33\_human 187 ---LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNTVALYVGIAV

DNA40628 775 AVLVLILLGILVFGIWFAYSRGHFDRT-KKGTSKKVIVSQP

\* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \* . \* \*  
A33\_human 244 GVVAALLIIGIIY---CCCCRGKDDNTEDKEDARPNEAYEEP

**FIG.- 10A**

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19  
 IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 112,12, FRAME = +1

DNA40628	112	LCSL--ALGSVTVSSEPEVRIPENNPKLSCAYSGFSSPR---VEW-KFDQGDTTRLVC	
SEQ ID NO:25		**.. . . . . * . . * . * . * . * . * . * . * . * . * . * . * . *	
A33 human	12	LCAVRTVDAISVETPQDDVLRASQQKSVTLPCTYHTSTSREGLIQWDKLLLTTERVV	
SEQ ID NO:26			
DNA40628	274	--YNNK--ITAS-YEDRVTFL-----PTGITFKSVTREDTGTYTCTMVSEEGGNSYGEVK	
		..** * * ..** . * . * . * . * . * . * . * . * . * . * . * . * . *	
A33 human	72	WPFSNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMS-DLEGNTK	
DNA40628	421	--VKLIVLVPPSKPTVNIPSSATIGNRAVLTCSSEQDGSPPEYTWFKDGIUMPTNPKSTR	
		* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *	
A33 human	131	SRVRLIILVPPSKPECIGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNINLQEQP---	
DNA40628	595	AFNSSSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPTMSNAVRMEAVERNVGV--	
		. * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *	
A33 human	187	-----LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNTVALYV	
DNA40628	766	-IVAAVLVTLILLGILVFGIFAYSRGHFDRT--KKGTSSKKVIRYSQP	
		* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *	
A33 human	240	GIAVGVVAALIIGIIY--CCCCRKGDDNTEDKEDARPNTREAYEEP	<b>FIG.- 10B</b>

SEQ ID NO: 6 A33\_hum 1 ..... M V G K W W P V L W T C A V R V T V D A I S V E T P Q D V I R A S O Q K S Y T L  
SEQ ID NO: 1 40628 1 W G T K A Q V E R K L L C L F I L A I L C S . . L A L G S V T V H S S E P E V R I P E N N P V K L

A33\_hum 42 P C T Y H T S S R E G L I O W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N A V S I  
40628 49 S C A Y S G F S S P R . . V E W . K F D O G D T T R L V C . . Y N N K . . I T A S . Y E D R V T F

A33\_hum 92 S N N A E Q S D A S I T I D Q L T W A D N G T Y E C S V S L W S D L E G N T K S V R L L V L V P P  
40628 90 . . . . . L P T G I T F K S V T R E D T G T Y T C H V S E E G G . N S Y G E V K Y K L L V L V P P

A33\_hum 142 S K P E C G I E G E T I I G N N I Q I L T C Q S K E G S P T P Q Y S W K R Y N I I L N O E Q P . . . .  
40628 133 S K P T V N I P S S A T I G N N A R V L T C S E O D G S P P S E Y T W F K D G U V W M P T N P K S T R A

A33\_hum 187 . . . . . L A Q P A S G Q P V S L K N I S I D T S G Y Y I C T S S N E E G T Q F C N I T V A V R S  
40628 183 F S N S S Y V L N P T G E . L V F D P L S A S D T G E Y S C E A R N G Y G T P W T S N A V R M E A

A33\_hum 231 P S M N V A L Y V G I A V G Y V A A L I I G I I Y C C . C C R G K D D N T E D K E D A R P N R E  
40628 232 V E R N V G V . . . I V A A V L V T I I L L G I L V F G I W F A Y S R G H F D A T K K G T S S K K V

A33\_hum 280 A Y E E P P E Q L R E L S R E E E D D Y R Q E E Q R S T G R E S P D H L D Q  
40628 279 I Y S O P S A R S E G E F K O T S S F L V

17 / 24

SEQ ID NO: 6 A33\_hum 1 **M V G K H W P V L W T L C A V R V T V D A I S V E T P Q D Y L R A S S Q G K S Y T P C T Y H T S T S**  
 SEQ ID NO: 2 45416 1 **. M G I L L G L L L G H L T V D I Y G R P I L E V P E S Y T G P W X G . D Y N L P C T Y D P L Q G**

A33\_hum 51 **S R E G L I Q W D K L L L T H T E R Y V I W . P F S N K N Y I H G E L Y K N R V S I S N N A E Q S D**  
 45416 49 **Y T Q V L V K W . L V Q R G S D P Y T I F L R D S S G D H I Q A K Y Q G R L H V S H K V . P G D**

A33\_hum 100 **A S I T I D Q I T H A D N G T Y E C S V S . L W S D L E G N T K S R V . . . . . R L L V L V P P S**  
 45416 96 **V S L Q I L S T L E M D D R S H Y T C E V T W Q T P D G N A V V R D K I T E L R V Q K L S V S K P T V**

A33\_hum 143 **K P E C G I E G E T I I G N N I Q L T C O S S K E G S P T P Q Y S W K R Y N I L N O E Q P L A O P A S**  
 45416 146 **T T G S G Y G F T V P Q G H R I S L O C A A R . G S P P P I S Y I W . Y K Q A T N N Q E P I K V A T**

A33\_hum 193 **G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T . Q F C N I . T V A V R S P S W N V A L Y V G**  
 45416 193 **L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E O H S D I V K F V V Y K D S S S K L L K T K T E**

A33\_hum 241 **I A V G V V A A L I I G I I I Y C C C C A R G K D D O N T E D K E D A R P N R E A Y E E P P E Q L R E**  
 45416 243 **A P T T W T Y P L K A T S T V K Q S W D W T T D W D G Y L G E T S A G P G K S L P V F A I I I S**

A33\_hum 291 **L S R E R E E E D D Y R O E E Q R A S T G R E E S P D H L D Q**  
 45416 293 **L C C H V V F T W A Y I W L C A K T S Q Q E H V Y E A A R**

FIG.- 13

SEQ ID NO: 6 A33\_hum 1 . . . W V G K H W P V [WT] C A V R Y T V D . . . A I S V E T P O D V L R A S O G K S V T L P C  
SEQ ID NO: 9 35638 1 M A R R S R H A L L [L] R Y L V V A L G Y H K A Y G F S A P K D Q Q V V T A V E Y Q E A I L A C

A33\_hum 44 T Y H T S T S R E G L I Q W D K I L L T H T E R V Y I W P F S N K N Y I H G E L Y K N R V S I S N  
35638 51 . . . K T P K K T V S S R L E W K K L . . . G R S Y S F V Y Y Q Q T . L Q G D . F K N R . . .

A33\_hum 94 N A E Q S D A S I T I D Q U L T M A D N G T Y E C S V S L M S D L E G N . T K S R V R I L L V P P S  
35638 87 . A E H I D F N I R I K N V T I R S D A G K Y R C E V S A P S E Q G O N L E E D T V T L E V L V A P A

A33\_hum 143 K P E C G I E G E T I I G N N I Q L T C O S K E G S P T P Q Y S W K R Y N I L N Q E O P L A O P A S  
35638 136 V P S C E V P S S A L S G T V V E L R A C Q D K E G N P A P E Y T W F K D G I R L L E N P R L G S Q S

A33\_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T O F C N I T V A Y . . . R S P S M N V A L Y V  
35638 186 T N S S Y T M N T K T G I L Q F N T . V S K L D T G E Y S C E A R N S V G Y R A C P G K R M O V D D

A33\_hum 240 G I A V G V V A L I I G I I I Y C C . . . C C R G K D D N T E D K E D A R P N R E A Y E E P P E  
35638 235 L N I S G I I A V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S N S S S K A T T

A33\_hum 287 Q L R E L S A . E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q  
35638 285 W S E N V Q O W L T P V I P A L W K A A A G G S R G C E F

19 / 24

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F T . S M I L C G S L V O G K G S Y Y T A Q S D V Q V P E N E S I K L T C  
SEQ ID NO: 1 40628 1 M G T K A Q V E R K L L C F I L A I I L C S L A L G S V T Y H S S E P E V R I P E N N P V K L S C

jam 50 T Y S G F S S P R A V E W K F V O G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S S V T  
40628 51 A Y S G F S S P R A V E W K F D O G D O T T R L V C Y N N K I T A S Y E D D R V T F L P T G I T F K S V T

jam 100 R K D N G E Y T C M Y S E E G G O N Y G E V S I H L T Y L V P P S K P T I S V P S S V T I G N R A V  
40628 101 R E D T G T Y T C M Y S E E G G N S Y G E V K V K L I Y L V P P S K P T V N I P S S A T I G N R A V

jam 150 L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F W N S S F T I D P K S G O L I F  
40628 151 L T C S E Q D G S P P S E Y T W F K D G I . V M P T N P K S T R A F S N S S Y V L N P T T G E L V E

jam 200 D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L N V G C I V A A V L V T L I L  
40628 200 D P L S A S D T G E Y S C E A R N G Y G T P W T S N A V R M E A V E R N V G V I V A A V L V T L I L

jam 250 L G L L I F G Y W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T A R S E G E F K Q T S S F L  
40628 250 L G I L V F G I W F A Y S R G H F D R T K K G T . S S K K V I Y S Q P S A R S E G E F K Q T S S F L

jam 300 V  
40628 299 V

FIG.-15

jam	49	C T Y S . . . C F S S P R V E W K F V O G S T T A L Y . . . C Y N S O I . T A P Y A D R V T F S .
45416	41	C T Y O P L A G Y T O V L Y X W I V O R G S O P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H

jam	90	...SSGIFTSSYTKDNGEYTCMV...SEE <del>G</del> ONYGEVSIH <del>T</del> YL·VPP
45416	91	KVPGOVSILOLSTLEMODASHYTCEV <del>T</del> WATPGNOVVRDOKITELRAYAKLSV

jam	132	S K P T I S V P S . . . . S V T I G N R A V L T C S E H D G S P P S E Y S W F X D G I S H L T A D A
45416	141	S K P T V T T G S G Y G F T V P O C H A I S L O C Q A R . G S P P S Y - W Y X Q O T N . . N Q E P

jam	178	K K T R A F H N S S F T I D P K S G D L I F D P V T A F D S G E Y C O A Q N G Y G T A M R S E A A
45416	188	I K V A T L . . . . . S T L L F X P A D S G S Y F C T A K G O V G S E O H S D I V

jam	228	H . . . H O A V E L N Y G G I V A A V L V T L L G L L I F G . . . V W F A Y S R G Y F E T T K K
45446	227	K F V V K O S S K U L K T K T E A P T M T Y P L K A T S T V K O S S W D W T T D M D G Y L G E I S A

jam 272 G T A P G K X K Y I Y S A P S T R A S E G E F K O T S S F L Y  
45416 277 G P G K S L P Y F A I L I I S L C M V V F T W A Y I H L C R A K T S O O E H V Y E A R

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S H I L G S L V Q C K G S V Y T A Q S D V O V . . . P E N E S I K L  
SEQ ID NO: 29 35638 1 . . . M A R R S R H A R L L L L L R Y L V V A L G Y H X A Y G F S A P X D Q Q V V T A V E Y Q E A I L

jam 48 T C . T Y S G F S S P R V E W K F V O G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S  
35638 49 A C K T P K K T V S S R L E W K K L . G R S V S F V Y Y Q A T L Q G D F K N R A E W I D F N J I R I K

jam 97 S V T R K D N G E Y T C H V S . . E E G G Q N Y G E V S I H L T Y L V P P S K P T I S V P S S V T I  
35638 98 N V T R S D A G K Y R A C E Y S A P S E Q Q N L E E D T V T L E V L V A P A V P S C E Y P S S S A L S

jam 145 G N R A V Y L T C S E H D G S P P S E Y S W F K D G I S M U T A D A K K T R A F M N S S F T I D P K S  
35638 148 G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L . E N P R L G S Q S T N S Y T M N T K T

jam 195 G O L I F D P Y T A F D S G E Y Y C O A O N G Y G T A M R S E A A H M D A V E L N V G G I V A A V L  
35638 197 G T L Q F N T V S K L D T G E Y S C E A R N S V G . Y R A C P G K R M Q V D D L N I S G I I A A V V

jam 245 Y T L I L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S O P S T R S E G E F K Q  
35638 246 Y V A L V I S V C G I G V C Y A Q R K G Y F . . . S K E T S F O K S N S S S K A T T M S E N V Q W L

jam 295 T S S F L V  
35638 293 T P V I P A L W K A A A G G S A G Q E F

**FIG.-17**

SEQ ID NO: 6	A33_hum	1	.....	W V G K W W P V L W T . L C A V R V T V D A I S V E T P Q O V L R A S Q G K S V T L P C T
SEQ ID NO: 10	jam	1	W G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D V Q V P E N E S I K L T C T	
A33_hum		45	Y H T S T S S R E G L I Q W D K L L T H T E R V V I W P F S N K N Y I H G E L Y K N A V S I S N N	
jam		51	Y S G F S S P R . . . Y E W . K F V Q G S T T A L V C . . Y N S Q . . IT A P . Y A D R V T F S S .	
A33_hum		95	A E Q S D O A S I T I D Q L T W A D N G T Y E C S V S L W S D O L E G N T K S R V R L L V L V P P S K P	
jam		91	... . . . S C I T F S S V T R K D N G E Y T C H V S E E G G . Q N Y G E V S I H L T V L V P P S K P	
A33_hum		145	E C G I E G E T I I G N N I Q O L T C A S K E G S P T P Q Y S W K R Y N I L N Q E Q P L A Q P A S G Q	
jam		135	T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M I L T A D A K K T R A F H	
A33_hum		195	P V S L K N I S T D T S G Y Y I C T S S N E E G T O F C N . . . I T V A V R S P S M N . . . V A L	
jam		185	N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L	
A33_hum		238	Y V . G I A V G V V A A L I I G I I - Y C . . . C C C A G K D D N T E D A R P N R E A Y E E	
jam		235	N Y G G I V A A V L V T L I I L G L L I F G V W F A Y S R G Y F E . I T K K G T A P G K K V I Y S Q	
A33_hum		284	P P E O L R E L S R E R E E E D O Y R Q E E Q R S T G R E S P D H L D Q	
jam		284	P S T A S E G E F K Q T S S F L V	

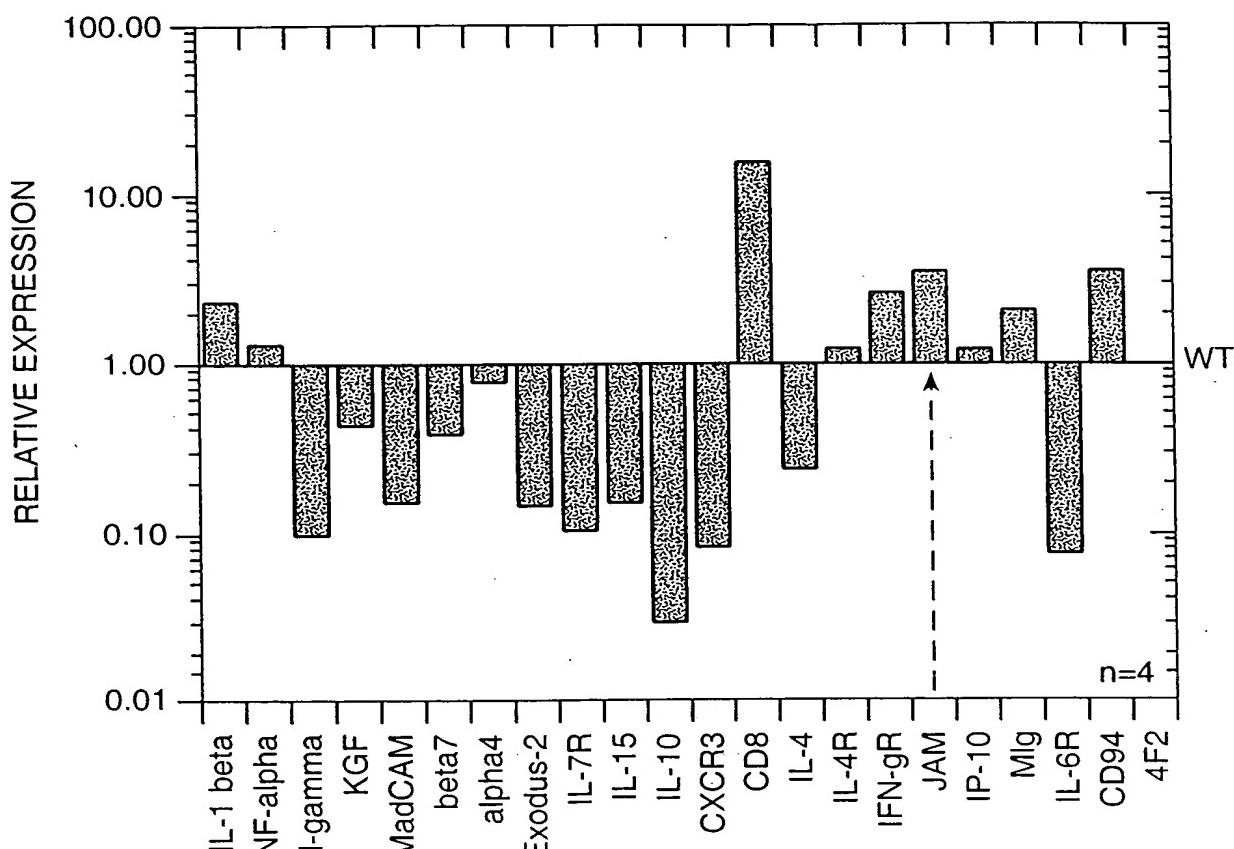
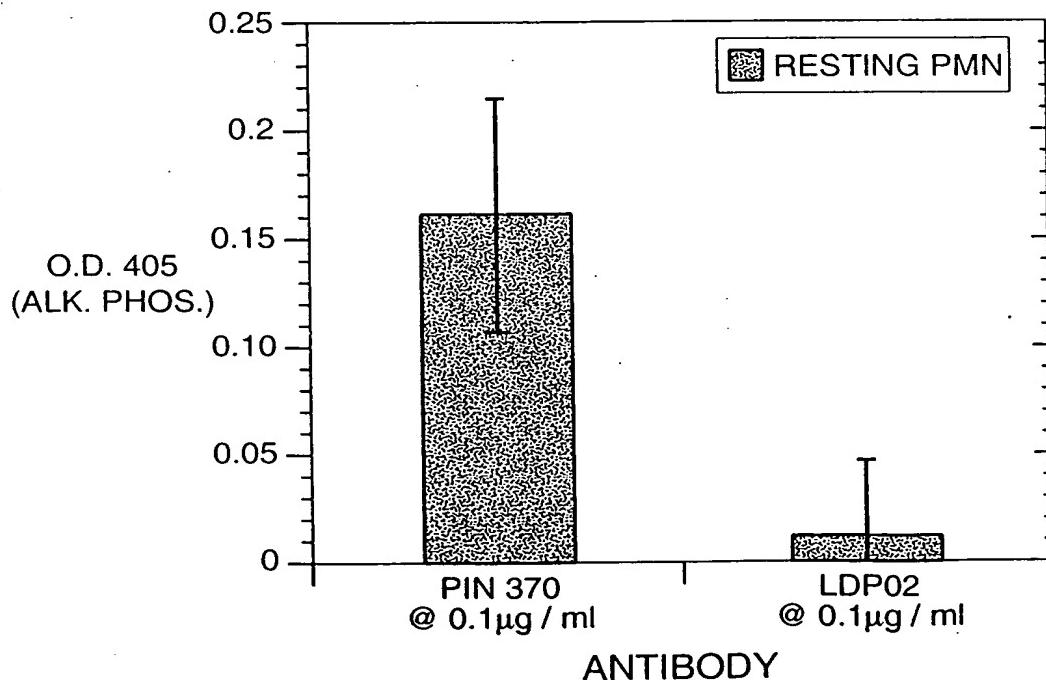
FIG.\_18

<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++	APPENDIX	+
PUTAMEN	+	OVARY	+++	LUNG	++++
SUSTANTIA NIGRA	+	PANCREAS	++	TRACHEA	++++
TEMPORAL LOBE	+	PITUITARY GLAND	++	PLACENTA	++++
THALAMUS	+	ADRENAL GLAND	++		
NUCLEUS ACCUMBENS	+	THYROID GLAND	++	FETAL BRAIN	+
SPINAL CORD	-	SALIVARY GLAND	+++	FETAL HEART	+
		MAMMARY GLAND	++	FETAL KIDNEY	++
				FETAL LIVER	+++
				FETAL SPLEEN	+
				FETAL LUNG	++++

23 / 24

FIG. 19

24 / 24

**FIG.\_20****FIG.\_21**